THE PENDING CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (currently amended) A method of detecting typable loci of a genome, comprising the steps of:

(a) amplifying genomic DNA with a population of random primers, thereby providing an amplified representative population of genome fragments comprising said typable loci, wherein said population comprises a high complexity representation;

(b) contacting said amplified representative population of genome fragments with a plurality of nucleic acid probes having sequences corresponding to said typable loci under conditions wherein probe-fragment hybrids are formed, wherein said amplified representative population of genome fragments comprises sequences identical to at least 90% of the genome, wherein said probes are at most 125 nucleotides in length, wherein said nucleic acid probes are immobilized on a substrate; and

(c) detecting typable loci of said probe-fragment hybrids.

2. (currently canceled)

3. (original) The method of claim 1, wherein said providing in step (a) comprises representationally amplifying a native genome.

4. (original) The method of claim 3, wherein said representationally amplifying comprises using a polymerase of low processivity.

5. (original) The method of claim 3, wherein said low processivity is less than 100 bases per polymerization event.

6. (original) The method of claim 3, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

7. (original) The method of claim 3, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

8. (previously canceled)

9. (currently amended) The method of claim 1 [8], wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

10. (original) The method of claim 1, wherein at least 100 typable loci are simultaneously detected.

11. (original) The method of claim 1, wherein said genome is a human genome.

12. (original) The method of claim 1, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

13. (previously presented) The method of claim 12, further comprising contacting said array of nucleic acid probes with chaperone probes.

14. (original) The method of claim 1, wherein said probes comprise nucleic acid probes that are at least 20 nucleotides in length.

15. (original) The method of claim 1, further comprising producing a report identifying said typable loci that are detected.

16. (previously canceled)

17. (original) The method of claim 1, wherein step (c) comprises directly detecting said typable loci of said fragments that hybridize to said probes.

18. (currently amended) A method of detecting typable loci of a genome, comprising the steps of:

(a) amplifying genomic DNA with a population of random primers, thereby providing an amplified representative population of genome fragments comprising said typable loci;

(b) contacting said amplified representative population of genome fragments with a plurality of nucleic acid probes having sequences corresponding to said typable loci under conditions wherein probe-fragment hybrids are formed, wherein said amplified representative population of genome fragments comprises sequences identical to at least 90% of the genome, wherein said nucleic acid probes are immobilized on a substrate; and

(c) directly detecting typable loci of said probe-fragment hybrids.

19. (previously presented) The method of claim 18, wherein at most 1000 copies of said genome are amplified.

20. (currently canceled)

21. (original) The method of claim 18, wherein said plurality of nucleic acid probes has sequences for typable loci linked to at least 5% of the expressed sequences of said genome.

22. (original) The method of claim 18, wherein said providing in step (a) comprises representationally amplifying a native genome.

23. (original) The method of claim 22, wherein said representationally amplifying comprises using a polymerase of low processivity.

24. (original) The method of claim 22, wherein said low processivity is less than 100 bases per polymerization event.

25. (original) The method of claim 22, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

26. (original) The method of claim 22, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

27. (previously canceled)

28. (original) The method of claim 18, wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

29. (original) The method of claim 18, wherein at least 100 typable loci are simultaneously detected.

30. (original) The method of claim 18, wherein said genome is a human genome.

31. (original) The method of claim 18, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

32. (original) The method of claim 31, further comprising contacting said array of nucleic acid probes with chaperone probes.

33. (previously presented) The method of claim 18, wherein said probes comprise nucleic acid probes that are at least 20 nucleotides in length.

34. (previously presented) The method of claim 18, further comprising producing a report identifying said typable loci that are detected.

35. (previously canceled)

36. (original) The method of claim 18, wherein step (c) comprises directly detecting said typable loci of said fragments that hybridize to said probes.

37. (currently amended) A method of detecting typable loci of a genome, comprising the steps of:

(a) amplifying genomic DNA with a population of random primers, thereby providing an amplified representative population of genome fragments comprising said typable loci, wherein said population of amplified genome fragments comprises a high complexity representation;

(b) contacting said amplified representative population of genome fragments with a plurality of immobilized nucleic acid probes having sequences corresponding to said typable loci under conditions wherein immobilized probe-fragment hybrids are formed;

(c) modifying said immobilized probe-fragment hybrids, wherein said modifying comprises incorporation of one or more nucleotides or nucleotide analogs in the probes or fragments of said probe-fragment hybrids; and

(d) detecting a probe or fragment modified in step (c), thereby detecting said typable loci of said genome.

38. (original) The method of claim 37, wherein said plurality of nucleic acid probes has sequences for typable loci linked to at least 10% of the expressed sequences of said genome.

39. (original) The method of claim 37, wherein said providing in step (a) comprises representationally amplifying a native genome.

40. (original) The method of claim 39, wherein said representationally amplifying comprises using a polymerase of low processivity.

41. (original) The method of claim 39, wherein said low processivity is less than 100 bases per polymerization event.

42. (original) The method of claim 39, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

43. (original) The method of claim 39, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

44. (original) The method of claim 37, wherein said nucleic acid probes are immobilized on a substrate.

45. (original) The method of claim 44, wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

46. (original) The method of claim 37, wherein at least 100 typable loci are simultaneously detected.

47. (original) The method of claim 37, wherein said genome is a human genome.

48. (original) The method of claim 37, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

49. (original) The method of claim 48, further comprising contacting said array of nucleic acid probes with chaperone probes.

50. (original) The method of claim 37, wherein said probes comprises nucleic acid probes are at least 20 nucleotides in length.

51. (original) The method of claim 37, further comprising producing a report identifying said typable loci that are detected.

52. (previously canceled)

53. (original) The method of claim 37, wherein step (c) comprises a primer extension assay.

54. (original) The method of claim 53, wherein said primer extension assay is selected from the group consisting of allele specific primer extension (ASPE), single base extension (SBE) and pyrosequencing.

55-63 (previously canceled)

64. (currently amended) A method for detecting typable loci of a genome, comprising the steps of

(a) in vitro transcribing a population of amplified genome fragments, thereby obtaining genomic RNA fragments, wherein said population of amplified genome fragments is produced by amplification with a plurality of random primers, wherein said population of amplified genome fragments comprises a high complexity representation;

(b) hybridizing said genomic RNA fragments with a plurality of immobilized nucleic acid probes having sequences corresponding to said typable loci, thereby forming a plurality of immobilized RNA fragment-probe hybrids;

(c) modifying said immobilized probe-fragment hybrids, wherein said modifying comprises incorporation of one or more nucleotides or nucleotide analogs in the probes or fragments of said probe-fragment hybrids; and

(d) [(c)] detecting typable loci of said RNA fragment-probe hybrids.

65. (previously canceled)

66. (original) The method of claim 64, wherein step (c) comprises modifying said genomic RNA fragment-probe hybrids with reverse transcriptase.

67. (original) The method of claim 66, wherein said modifying comprises replicating said genomic RNA fragments hybridized in said genomic RNA fragment-probe hybrids with a

plurality of different locus-specific primers, thereby producing a locus-specific, amplified representative population of genome fragments.

68. (original) The method of claim 67, wherein step (a) comprises in vitro transcribing said population of amplified genome fragments using random primers comprising a 3' sequence region that is random and another sequence region having a constant sequence, thereby obtaining genomic RNA fragments labeled with said constant sequence.

69. (original) The method of claim 68, wherein said locus-specific primers comprise a 3' sequence region that is locus-specific and a another sequence region having a second constant sequence, thereby obtaining genomic RNA fragments labeled with said first constant region and said second constant region.

70. (original) The method of claim 69, further comprising a step of replicating the genomic RNA fragments with complementary primers to the first constant region and second constant region.

71. (original) The method of claim 66, wherein said modifying said genomic RNA fragment-probe hybrids with reverse transcriptase occurs under conditions wherein DNA-dependent DNA synthesis is inhibited.

72. (original) The method of claim 64, further comprising a step of isolating said genomic RNA fragments.

73-77 (previously canceled)

78. (previously presented) The method of claim 1, wherein said genomic DNA is amplified under isothermal conditions using a polymerase having strand displacing activity.

79. (previously presented) The method of claim 18, wherein said genomic DNA is amplified under isothermal conditions using a polymerase having strand displacing activity.

80. (previously presented) The method of claim 37, wherein said genomic DNA is amplified under isothermal conditions using a polymerase having strand displacing activity.

81. (new) The method of claim 37, wherein said modifying in step (c) comprises ligation.

82. (new) The method of claim 37, wherein said modifying in step (c) comprises extension-ligation.